IN THE CLAIMS

1) (currently amended) A computer readable medium having computer-executable instructions that when executed by a computer cause the computer to perform a method for determining an optimal test order for diagnosing mutations that relate to a disease, the method comprising:

a) receiving data indicative of a historical frequency distribution of mutations that relate to the disease and the assays required to diagnose the mutations that relate to the disease;

b) creating a history database, the database comprising a sequence of records based on the data;

c) receiving new data indicative of the historical frequency distribution of mutations that relate to the disease and the assays required to diagnose the mutations that relate to the disease

d) applying at least one decision tree algorithm, wherein the at least one decision tree algorithm comprises: (i) accessing a set of records with the history database; (ii) generating at least two strategies from the accessed records; and (iii) ranking the at least two strategies by calculating the strategy expected cost for each of the at least two strategies; and

e) identifying the optimal test order as the strategy with the lowest strategy expected cost

2) (currently amended) The computer readable medium of claim 1, wherein the strategy expected cost is calculated using the formula:

$$Strategy\ Expected\ Cost = \sum_{j=1}^{N} p_j \sum_{i=1}^{T_j} \left(C_{ij} - B_{ij} \right)$$

where Cij is a cost of the i'th action performed along a j'th feasible search path; Bij is the value of all incremental benefits attained by the i'th action performed along the j'th feasible search path; Tj is the total number of actions on search path j; N is the number of feasible search paths

generated by a particular strategy; and pj is the likelihood that the search path j occurs and is approximated by the frequency distribution of empirically observed outcomes.

3) (canceled)

4) (currently amended) A system for determining an optimal test order for diagnosing mutations that relate to a disease, comprising:

a) a computing environment;

b) an input device, connected to the computing environment for receiving data;

c) receiving data;

d) an output device, connected to the computing environment, for presenting data; and

e) at least one decision tree algorithm executed based on at least a portion of the data received from the input device, wherein the at least one decision tree algorithm ranks at least a portion of the data and determines the optimal test order associated with the at least one decision tree algorithm, wherein the optimal test order is presented via the output device.

5) (currently amended) The system of claim 4, wherein the at least one decision tree algorithm further determines a projected cost for each test associated with the optimal test order, wherein the projected cost is presented via the output device.

6) (currently amended) The system of claim 5, wherein the received data comprises the historical frequency distribution of mutations that relate to the disease and the assays required to diagnose the mutations that relate to the disease.

7) (currently amended) The system of claim 6, wherein the at least one decision tree algorithm is specific to hereditary diseases selected from the group consisting of breast cancer, colorectal cancer, lung cancer, prostate cancer, retinoblastoma, and hereditary hemorrhagic telangiectasia.

8) (currently amended) The system of claim 7, wherein the decision tree consists of at least two strategies.

9) (currently amended) The system of claim 8, wherein the at least two strategies are ranked by projected cost.

10) (currently amended) The system of claim 9, wherein the at least two strategies comprise at least two assays.

11) (currently amended) The system of claim 10, wherein the at least two strategies are ranked based on minimum projected cost to perform the at least two medical diagnostic assays.

12) (currently amended) A method of determining the optimal test order for diagnosing mutations that relate to a disease, comprising:

a) receiving data indicative of a historical frequency distribution of mutations that relate to the disease and the assays required to diagnose the mutations that relate to the disease;

b) creating a history database, the database comprising a sequence of records based on the data;

c) receiving new data indicative of the historical frequency distribution of mutations that relate to the disease and the assays required to diagnose the mutations that relate to the disease;

d) applying at least one decision tree algorithm, wherein the at least one decision tree algorithm scores at least a portion of the new data; and

e) generating a recommendation if the score satisfies a threshold.

13) (currently amended) The method of claim 12, wherein applying at least one decision tree algorithm comprises:

a) accessing a set of records within the history database;

b) generating at least two strategies from the accessed records;

c) comparing the at least two strategies against each other; and

d) calculating the projected cost for the at least two ~~strategy~~ strategies identified by the comparing step.

14) (original) The method of claim 13 wherein the projected cost is calculated from a pre-selected minimum number of records within the history database.

15) (canceled)

16) (canceled)

17) (canceled)

18) (canceled)

19) (new) A method of determining a minimal cost test order for diagnosing mutations that relate to a disease, comprising:

(a) generating a data set comprised of data obtained by:

identifying a spectrum of mutations that relate to the disease and the frequency with which each mutation occurs in the population;

for each mutation in the population, identify a set of assays that provide a diagnosis;

for each assay, identifying the average cost of each assay; and

for each assay performed, identifying the probability of a successful diagnosis wherein the probability of a successful diagnosis is the benefit of the diagnosis,

(b) maintaining the data set to include new data received on the spectrum of mutations that relate to the disease, the frequency with which each mutation occurs in the population and the set of assays that provide a diagnosis;

(c) applying at least one decision tree algorithm to the data, wherein the at least one decision tree algorithm comprises: (i) generating at least two strategies using the assays within the data set; (ii) ranking the at least two strategies by calculating the strategy expected cost of the at least two assays,

wherein the strategy expected cost is determined using the formula

$$Strategy\ Expected\ Cost = \sum_{j=1}^{N} p_j \sum_{i=1}^{T_j} \left(C_{ij} - B_{ij} \right)$$

where C_{ij} is the cost of a i'th action performed along a j'th feasible search path; B_{ij} is the value of all incremental benefits attained by the i'th action performed along the j'th feasible search path; T_j is the total number of actions on the search path j; N is the number of feasible search paths generated by a particular strategy; and p_j is the likelihood that the search path j occurs and is approximated by the frequency distribution of empirically observed outcomes; and

(iii) identifying, from the ranked at least two strategies, the at least one strategy with the lowest strategy expected cost.

20) (new) The method of claim 19, wherein a subsequent lowest strategy expected cost is obtained using an arbitrary initial assay or assays from the set of assays.

21) (new) The method of claim 20 or 21, wherein the optimal test order is determined using the equation

$$\frac{q_i(h)}{C_i} < \frac{1}{B}$$

where $q_i(h)$ is the probability that a diagnosis is achieved by any combination of the assays not yet performed, given history (h), B represents the benefit of a conclusive diagnosis

and by terminating the at least one strategy with the lowest strategy expected cost when the expected cost exceeds the benefit of a conclusive diagnosis.